SEQUENCE LISTING

<110> PARANHOS-BACCALA, Glaucia

KOMURIAN-PRADEL, Florence

BEDIN, Frederic

SODOYER, Mireille

OTT, Catherine

MALLET, Francois

PERRON, Herve

MANDRAND, Bernard

<120> RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR DIAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC USES

<130> 103514

<140> US/09/319,156

<141> 1999-11-02

<150> PCT/FR98/01460

<151> 1998-07-07

<150> FR/97/08816

<151> 1997-07-07

<160> 45

<170> PatentIn version 3.1

1

<210> 1

<211> 34

<212> DNA

<213> MSRV

<400> 1
gactcgctgc agatcgattt tttttttttt tttt   34

<210> 2

<211> 30

<212> DNA

<213> MSRV

<400> 2
gccatcaagc cacccaagaa ctcttaactt   30

<210> 3

<211> 30

<212> DNA

<213> MSRV

<400> 3
ccaatagcca gaccattata tacactaatt   30

<210> 4

<211> 310

<212> DNA

<213> MSRV

<400> 4
gcttatagaa ggacccctag tatggggtaa tcccctctgg gaaaccaagc cccagtactc   60

agcaggaaaa atagaatagg aaacctcaca aggacatact ttcctcccct ccagatggct   120

agccactgag gaaggaaaaa tactttcacc tgcagctaac caacagaaat tacttaaaac   180

2

ccttcaccaa accttccact taggcattga tagcacccat cagatggcca aattattatt   240

tactggacca ggccttttca aaactatcaa gaagatagtc aggggctgtg aagtgtgcca   300

aagaaataat   310

<210>   5

<211>   103

<212>   PRT

<213>   MSRV

<220>

<221>   misc_feature

<222>   (26)..(26)

<223>   Xaa = any amino acid

<400>   5

Leu Ile Glu Gly Pro Leu Val Trp Gly Asn Pro Leu Trp Glu Thr Lys
1   5   10   15

Pro Gln Tyr Ser Ala Gly Lys Ile Glu Xaa Glu Thr Ser Gln Gly His
            20   25   30

Thr Phe Leu Pro Ser Arg Trp Leu Ala Thr Glu Glu Gly Lys Ile Leu
        35   40   45

Ser Pro Ala Ala Asn Gln Gln Lys Leu Leu Lys Thr Leu His Gln Thr
    50   55   60

Phe His Leu Gly Ile Asp Ser Thr His Gln Met Ala Lys Leu Leu Phe
65   70   75   80

Thr Gly Pro Gly Leu Phe Lys Thr Ile Lys Lys Ile Val Arg Gly Cys
                85   90   95

Glu Val Cys Gln Arg Asn Asn
                100

3

<210> 6

<211> 635

<212> DNA

<213> MSRV

<400> 6

```
ccctgtatct ttaacctcct tgttaagttt gtctcttcca gaatcaaaac tgtaaaacta      60

caaattgttc ttcaaatgga gcaccagatg gagtccatga ctaagatcca ccgtggaccc     120

ctggaccggc ctgctagccc atgctccgat gttaatgaca ttgaaggcac ccctcccgag     180

gaaatctcaa ctgcacaacc cctactatgc cccaattcag cgggaagcag ttagagcggt     240

catcagccaa cctccccaac agcacttggg ttttcctgtt gagagggggg actgagagac     300

aggactagct ggatttccta ggccaacgaa gaatccctaa gcctagctgg aaggtgact      360

gcatccacct ctaaacatgg ggcttgcaac ttagctcaca cccgaccaat cagagagctc     420

actaaaatgc taattaggca aaaataggag gtaaagaaat agccaatcat ctattgcctg     480

agagcacagc gggagggaca aggatcggga tataaaccca ggcattcgag ccggcaacgg     540

caaccccctt tgggtccccct cccttttgtat gggcgctctg ttttcactct atttcactct     600

attaaatctt gcaactgaaa aaaaaaaaaa aaaaa                                 635
```

<210> 7

<211> 77

<212> PRT

<213> MSRV

<400> 7

```
Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile Lys
1                5                10               15
```
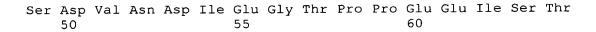
```
Thr Val Lys Leu Gln Ile Val Leu Gln Met Glu His Gln Met Glu Ser
            20               25               30
```

```
Met Thr Lys Ile His Arg Gly Pro Leu Asp Arg Pro Ala Ser Pro Cys
        35               40               45
```

4

Ser Asp Val Asn Asp Ile Glu Gly Thr Pro Pro Glu Glu Ile Ser Thr
    50   55   60

Ala Gln Pro Leu Leu Cys Pro Asn Ser Ala Gly Ser Ser
65   70   75

<210> 8

<211> 32

<212> DNA

<213> MSRV

<400> 8
tggggttcca tttgtaagac catctgtagc tt   32

<210> 9

<211> 1481

<212> DNA

<213> MSRV

<400> 9
atggccctcc cttatcatac ttttctcttt actgttctct tacccccttt cgctctcact   60

gcaccccctc catgctgctg tacaaccagt agctcccctt accaagagtt tctatgaaga   120

acgcggcttc ctggaaatat tgatgcccca tcatatagga gtttatctaa gggaaactcc   180

accttcactg cccacaccca tatgccccgc aactgctata actctgccac tctttgcatg   240

catgcaaata ctcattattg gacagggaaa atgattaatc ctagttgtcc tggaggactt   300

ggagccactg tctgttggac ttacttcacc cataccagta tgtctgatgg gggtggaatt   360

caaggtcagg caagagaaaa acaagtaaag gaagcaatct cccaactgac ccggggacat   420

agcacccctc gcccctacaa aggactagtt ctctcaaaac tacatgaaac cctccgtacc   480

catactcgcc tggtgagcct atttaatacc accctcactc ggctccatga ggtctcagcc   540

caaaacccta ctaactgttg gatgtgcctc cccctgcact tcaggccata catttcaatc   600

cctgttcctg aacaatggaa caacttcagc acagaaataa acaccacttc cgtttttagta   660

ggacctcttg tttccaatct ggaaataacc catacctcaa acctcacctg tgtaaaattt   720

agcaatacta tagacacaac cagctcccaa tgcatcaggt gggtaacacc tcccacacga   780

```
atagtctgcc taccctcagg aatatttttt gtctgtggta cctcagccta tcattgtttg    840

aatggctctt cagaatctat gtgcttcctc tcattcttag tgcccctat gaccatctac     900

actgaacaag atttatacaa tcatgtcgta cctaagcccc acaacaaaag agtacccatt    960

cttccttttg ttatcagagc aggagtgcta ggcagactag gtactggcat tggcagtatc   1020

acaacctcta ctcagttcta ctacaaacta tctcaagaaa taaatggtga catggaacag   1080

gtcactgact ccctggtcac cttgcaagat caacttaact ccctagcagc agtagtcctt   1140

caaaatcgaa gagctttaga cttgctaacc gccaaagag ggggaacctg tttattttta    1200

ggagaagaac gctgttatta tgttaatcaa tccagaattg tcactgagaa agttaaagaa   1260

attcgagatc gaatacaatg tagagcagag gagcttcaaa acaccgaacg ctggggcctc   1320

ctcagccaat ggatgccctg ggttctcccc ttcttaggac ctctagcagc tctaatattg   1380

ttactcctct ttggaccctg tatctttaac ctccttgtta gtttgtctc ttccagaatt    1440

gaagctgtaa agctacagat ggtcttacaa atggaacccc a                       1481


<210>  10

<211>  493

<212>  PRT

<213>  MSRV


<220>

<221>  misc_feature

<222>  (39)..(39)

<223>  Xaa = any amino acid


<400>  10

Met Ala Leu Pro Tyr His Thr Phe Leu Phe Thr Val Leu Leu Pro Pro
1               5                  10                  15


Phe Ala Leu Thr Ala Pro Pro Pro Cys Cys Cys Thr Thr Ser Ser Ser
            20                  25                  30


Pro Tyr Gln Glu Phe Leu Xaa Arg Thr Arg Leu Pro Gly Asn Ile Asp
        35                  40                  45
```

6

```
Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Asn Ser Thr Phe Thr Ala
    50              55              60

His Thr His Met Pro Arg Asn Cys Tyr Asn Ser Ala Thr Leu Cys Met
65              70              75              80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
            85              90              95

Pro Gly Gly Leu Gly Ala Thr Val Cys Trp Thr Tyr Phe Thr His Thr
            100             105             110

Ser Met Ser Asp Gly Gly Gly Ile Gln Gly Gln Ala Arg Glu Lys Gln
        115             120             125

Val Lys Glu Ala Ile Ser Gln Leu Thr Arg Gly His Ser Thr Pro Ser
    130             135             140

Pro Tyr Lys Gly Leu Val Leu Ser Lys Leu His Glu Thr Leu Arg Thr
145             150             155             160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Arg Leu His
            165             170             175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Met Cys Leu Pro Leu
            180             185             190

His Phe Arg Pro Tyr Ile Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
    195             200             205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val
    210             215             220

Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
225             230             235             240

Ser Asn Thr Ile Asp Thr Thr Ser Ser Gln Cys Ile Arg Trp Val Thr
            245             250             255

Pro Pro Thr Arg Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
            260             265             270
```

7

```
Gly Thr Ser Ala Tyr His Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
        275             280             285


Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
    290             295             300


Leu Tyr Asn His Val Val Pro Lys Pro His Asn Lys Arg Val Pro Ile
305             310             315             320


Leu Pro Phe Val Ile Arg Ala Gly Val Leu Gly Arg Leu Gly Thr Gly
                325             330             335


Ile Gly Ser Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
            340             345             350


Glu Ile Asn Gly Asp Met Glu Gln Val Thr Asp Ser Leu Val Thr Leu
        355             360             365


Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Gln Asn Arg Arg
    370             375             380


Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr Cys Leu Phe Leu
385             390             395             400


Gly Glu Glu Arg Cys Tyr Tyr Val Asn Gln Ser Arg Ile Val Thr Glu
            405             410             415


Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Cys Arg Ala Glu Glu Leu
            420             425             430


Gln Asn Thr Glu Arg Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Val
        435             440             445


Leu Pro Phe Leu Gly Pro Leu Ala Ala Leu Ile Leu Leu Leu Leu Phe
    450             455             460


Gly Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile
465             470             475             480


Glu Ala Val Lys Leu Gln Met Val Leu Gln Met Glu Pro
            485             490
```

<211> 32

<212> DNA

<213> MSRV

<400> 11
tcaaaatcga agagctttag acttgctaac cg   32

<210> 12

<211> 1329

<212> DNA

<213> MSRV

<220>

<221> misc_feature

<222> (594)..(594)

<223> n = a, g, c or t/u

<220>

<221> misc_feature
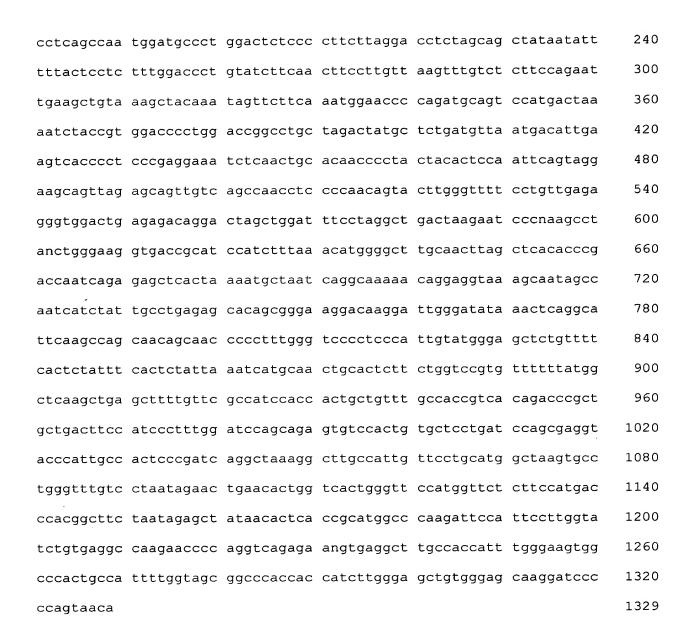
<222> (602)..(602)

<223> n = a, g, c or t/u

<220>

<221> misc_feature

<222> (1232)..(1232)

<223> n = a, g, c or t/u

<400> 12
tcaaaatcga agagctttag acttgctaac cgccaaaaga gggggaacct gtttattttt   60

aggggaagaa tgctgttagt atgttaatca atctggaatc attactgaga aagttaaaga   120

aatttgagat cgaatataat gtagagcaga ggaccttcaa aacactgcac cctggggcct   180

```
cctcagccaa tggatgccct ggactctccc cttcttagga cctctagcag ctataatatt      240

tttactcctc tttggaccct gtatcttcaa cttccttgtt aagtttgtct cttccagaat      300

tgaagctgta aagctacaaa tagttcttca aatggaaccc cagatgcagt ccatgactaa      360

aatctaccgt ggacccctgg accggcctgc tagactatgc tctgatgtta atgacattga      420

agtcacccct cccgaggaaa tctcaactgc acaacccta ctacactcca attcagtagg      480

aagcagttag agcagttgtc agccaacctc cccaacagta cttgggtttt cctgttgaga      540

gggtggactg agagacagga ctagctggat ttcctaggct gactaagaat cccnaagcct      600

anctgggaag gtgaccgcat ccatctttaa acatggggct tgcaacttag ctcacacccg      660

accaatcaga gagctcacta aaatgctaat caggcaaaaa caggaggtaa agcaatagcc      720

aatcatctat tgcctgagag cacagcggga aggacaagga ttgggatata aactcaggca      780

ttcaagccag caacagcaac ccccttтggg tccctccca ttgtatggga gctctgtttt      840

cactctattt cactctatta aatcatgcaa ctgcactctt ctggtccgtg tttttatgg      900

ctcaagctga gcttttgttc gccatccacc actgctgttt gccaccgtca cagacccgct      960

gctgacttcc atccctttgg atccagcaga gtgtccactg tgctcctgat ccagcgaggt     1020

acccattgcc actcccgatc aggctaaagg cttgccattg ttcctgcatg gctaagtgcc     1080

tgggtttgtc ctaatagaac tgaacactgg tcactgggtt ccatggttct cttccatgac     1140

ccacggcttc taatagagct ataacactca ccgcatggcc caagattcca ttccttggta     1200

tctgtgaggc caagaacccc aggtcagaga angtgaggct tgccaccatt tgggaagtgg     1260

cccactgcca ttttggtagc ggcccaccac catcttggga gctgtgggag caaggatccc     1320

ccagtaaca                                                            1329


<210>  13

<211>  162

<212>  PRT

<213>  MSRV


<220>

<221>  misc_feature

<222>  (26)..(26)
```

10

<223> Xaa = any amino acid

<220>

<221> misc_feature

<222> (42)..(42)

<223> Xaa = any amino acid

<220>

<221> misc_feature

<222> (46)..(46)

<223> Xaa = any amino acid

<400> 13

```
Gln Asn Arg Arg Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr
1               5                   10                  15

Cys Leu Phe Leu Gly Glu Glu Cys Cys Xaa Tyr Val Asn Gln Ser Gly
            20                  25                  30

Ile Ile Thr Glu Lys Val Lys Glu Ile Xaa Asp Arg Ile Xaa Cys Arg
            35                  40                  45

Ala Glu Asp Leu Gln Asn Thr Ala Pro Trp Gly Leu Leu Ser Gln Trp
    50                  55                  60

Met Pro Trp Thr Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Phe
65                  70                  75                  80

Leu Leu Leu Phe Gly Pro Cys Ile Phe Asn Phe Leu Val Lys Phe Val
                85                  90                  95

Ser Ser Arg Ile Glu Ala Val Lys Leu Gln Ile Val Leu Gln Met Glu
                100                 105                 110

Pro Gln Met Gln Ser Met Thr Lys Ile Tyr Arg Gly Pro Leu Asp Arg
            115                 120                 125
```

11

```
Pro Ala Arg Leu Cys Ser Asp Val Asn Asp Ile Glu Val Thr Pro Pro
    130                 135                 140


Glu Glu Ile Ser Thr Ala Gln Pro Leu Leu His Ser Asn Ser Val Gly
145                 150                 155                 160


Ser Ser


<210>  14

<211>  21

<212>  DNA

<213>  MSRV


<400>  14
ggcattgata gcacccatca g                                              21


<210>  15

<211>  21

<212>  DNA

<213>  MSRV


<400>  15
catgtcacca gggtggaata g                                              21


<210>  16

<211>  758

<212>  DNA

<213>  MSRV


<400>  16
ggcattgata gcacccatca gatggccaaa tcattattta ctggaccagg ccttttcaaa    60

actatcaagc agatagggcc cgtgaagcat gccaaagaaa taatcccctg ccttatcgcc   120

atgttccttc aggagaacaa agaacaggcc attacccagg ggaagactgg caactagatt   180

ttacccacat ggccaaatgt cagggatttc agcatctact agtctgggca gatactttca   240
```

12

```
ctggttgggt ggagtcttct ccttgtagga cagaaaagac ccaagaggta ataaaggcac        300

taatgaaata attcccagat ttggacttcc cccaggatta cagggtgaca atggccccgc        360

tttcaaggct gcagtaaccc agggagtatc ccaggtgtta ggcatacaat atcacttaca        420

ctgtgcctgg aggccacaat cctccagaaa agtcaagaaa atgaatgaaa cactcaaaga        480

tctaaaaaag ctaacccaag aaacccacat tgcatgacct gttctgttgc ctataacctt        540

actaagaatc cataactatc ccccaaaaag caggacttag cccatacgag atgctatatg        600

gatggccttt cctaaccaat gaccttgtgc ttgactgaga aatggccaac ttagttgcag        660

acatcacctc cttagccaaa tatcaacaag ttcttaaaac atcacaggga acctgtcccc        720

gagaggaggg aaaggaacta ttccaccctg gtgacatg                                 758
```

\<210\> 17

\<211\> 25

\<212\> DNA

\<213\> MSRV

\<400\> 17
```
cggacatcca aagtgatggg aaacg                                                 25
```

\<210\> 18

\<211\> 26

\<212\> DNA

\<213\> MSRV

\<400\> 18
```
ggacaggaaa gtaagactga gaaggc                                                26
```

\<210\> 19

\<211\> 26

\<212\> DNA

\<213\> MSRV

<400> 19
cctagaacgt attctggaga attggg   26

<210> 20

<211> 26

<212> DNA

<213> MSRV

<400> 20
tggctctcaa tggtcaaaca tacccg   26

<210> 21

<211> 1511

<212> DNA

<213> MSRV.

<400> 21
cctagaacgt attctggaga attgggacca atgtgacact cagacgctaa gaaagaaacg   60

atttatattc ttctgcagta ccgcctggcc acaatatcct cttcaaggga gagaaacctg   120

gcttcctgag ggaagtataa attataacat catcttacag ctagacctct tctgtagaaa   180

ggagggcaaa tggagtgaag tgccatatgt gcaaactttc ttttcattaa gagacaactc   240

acaattatgt aaaaagtgtg gtttatgccc tacaggaagc cctcagagtc cacctcccta   300

ccccagcgtc ccctccccga ctccttcctc aactaataag gaccccctt taacccaaac   360

ggtccaaaag gagatagaca aaggggtaaa caatgaacca aagagtgcca atattccccg   420

attatgcccc ctccaagcag tgagaggagg agaattcggc ccagccagag tgcctgtacc   480

tttttctctc tcagacttaa agcaaattaa aatagaccta ggtaaattct cagataaccc   540

tgacggctat attgatgttt tacaagggtt aggacaatcc tttgatctga catggagaga   600

tataatgtta ctactaaatc agacactaac cccaaatgag agaagtgccg ctgtaactgc   660

agcccgagag tttggcgatc tttggtatct cagtcaggcc aacaatagga tgacaacaga   720

ggaaagaaca actcccacag gccagcaggc agttcccagt gtagaccctc attgggacac   780

agaatcagaa catggagatt ggtgccacaa acatttgcta acttgcgtgc tagaaggact   840

gaggaaaact aggaagaagc ctatgaatta ctcaatgatg tccactataa cacagggaaa   900

ggaagaaaat cttactgctt ttctggacag actaagggag gcattgagga agcatacctc   960

cctgtcacct gactctattg aaggccaact aatcttaaag gataagttta tcactcagtc   1020

agctgcagac attagaaaaa acttcaaaag tctgccttag gcccggagca gaacttagaa   1080

accctatttta acttggcatc ctcagttttt tataatagag atcaggagga gcaggcgaaa   1140

cgggacaaac gggataaaaa aaaaagggg ggtccactac tttagtcatg gccctcaggc   1200

aagcagactt tggaggctct gcaaaaggga aagctgggc aaatcaaatg cctaataggg   1260

ctggcttcca gtgcggtcta caaggacact ttaaaaaaga ttatccaagt agaaataagc   1320

cgccccttg tccatgcccc ttacgtcaag ggaatcactg gaaggcccac tgccccaggg   1380

gatgaagata ctctgagtca gaagccatta accagatgat ccagcagcag gactgagggt   1440

gcccgggggcg agcgccagcc catgccatca ccctcacaga gccccgggta tgtttgacca   1500

ttgagagcca a   1511

<210>   22

<211>   352

<212>   PRT

<213>   MSRV

<400>   22

Leu Glu Arg Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr Leu
1   5   10   15

Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln Tyr
            20   25   30

Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr
        35   40   45

Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp
    50   55   60

Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser
65   70   75   80

Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser
                85   90   95

15

Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn
        100   105   110

Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly
        115   120   125

Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu
    130   135   140

Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro
145   150   155   160

Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe
            165   170   175

Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln
            180   185   190

Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr
        195   200   205

Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe
    210   215   220

Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu
225   230   235   240

Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro
            245   250   255

His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu
            260   265   270

Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met
            275   280   285

Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu
        290   295   300

Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser
305   310   315   320

16

```
Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe
                325                 330                 335


Ile Thr Gln Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu Pro
                340                 345                 350
```

<210> 23

<211> 30

<212> DNA

<213> MSRV

<400> 23
tgctggaatt cgggatccta gaacgtattc   30

<210> 24

<211> 30

<212> DNA

<213> MSRV

<400> 24
agttctgctc cgaagcttag gcagactttt   30

<210> 25

<211> 398

<212> PRT

<213> MSRV

<400> 25

```
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
1               5                   10                  15


Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
                20                  25                  30


Ile Leu Glu Arg Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr
        35                  40                  45
```

```
Leu Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln
    50              55              60

Tyr Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn
65              70              75                      80

Tyr Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys
            85              90              95

Trp Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn
            100             105             110

Ser Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln
        115             120             125

Ser Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr
    130             135             140

Asn Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys
145             150             155             160

Gly Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro
            165             170             175

Leu Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val
        180             185             190

Pro Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys
    195             200             205

Phe Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly
    210             215             220

Gln Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln
225             230             235             240

Thr Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu
            245             250             255

Phe Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr
            260             265             270
```

18

```
Glu Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp
        275             280              285

Pro His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His
    290             295              300

Leu Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro
305              310              315              320

Met Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn
            325              330              335

Leu Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr
        340              345              350

Ser Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys
    355              360              365

Phe Ile Thr Gln Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu
    370              375              380

Pro Lys Leu Ala Ala Ala Leu Glu His His His His His His
385              390              395
```

<210> 26

<211> 378

<212> PRT

<213> MSRV

<400> 26

```
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Leu Glu Arg
1               5               10              15

Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr Leu Arg Lys Lys
            20              25              30

Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln Tyr Pro Leu Gln
        35              40              45

Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr Asn Ile Ile
    50              55              60
```

Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp Ser Glu Val
65   70   75   80

Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser Gln Leu Cys
                85   90   95

Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser Pro Pro Pro
            100   105   110

Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn Lys Asp Pro
        115   120   125

Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly Val Asn Asn
    130   135   140

Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu Gln Ala Val
145   150   155   160

Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro Phe Ser Leu
                165   170   175

Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe Ser Asp Asn
            180   185   190

Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln Ser Phe Asp
        195   200   205

Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr Leu Thr Pro
    210   215   220

Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe Gly Asp Leu
225   230   235   240

Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu Glu Arg Thr
                245   250   255

Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro His Trp Asp
            260   265   270

Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu Leu Thr Cys
        275   280   285

20

Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met Asn Tyr Ser
    290   295   300

Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu Thr Ala Phe
305   310   315   320

Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser Leu Ser Pro
                325   330   335

Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe Ile Thr Gln
                340   345   350

Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu Pro Lys Leu Ala
            355   360   365

Ala Ala Leu Glu His His His His His His
    370   375

<210> 27

<211> 25

<212> DNA

<213> MSRV

<400> 27
cttggagggt gcataaccag ggaat   25

<210> 28

<211> 20

<212> DNA

<213> MSRV

<400> 28
tgtccgctgt gctcctgatc   20

<210> 29

<211> 25

<212> DNA

<213> MSRV

<400> 29
ctatgtcctt ttggactgtt tgggt   25

<210> 30

<211> 764

<212> DNA

<213> MSRV

<400> 30
tgtccgctgt gctcctgatc cagcacaggc gcccattgcc tctcccaatt gggctaaagg   60

cttgccattg ttcctgcaca gctaagtgcc tgggttcatc ctaatcgagc tgaacactag   120

tcactgggtt ccacggttct cttccatgac ccatggcttc taatagagct ataacactca   180

ctgcatggtc caagattcca ttccttggaa tccgtgagac caagaacccc aggtcagaga   240

acacaaggct tgccaccatg ttggaagcag cccaccacca ttttggaagc agcccgccac   300

tatcttggga gctctgggag caaggacccc aggtaacaat ttggtgacca cgaagggacc   360

tgaatccgca accatgaagg gatctccaaa gcaattggaa atgttcctcc caaggcaaaa   420

atgcccctaa gatgtattct ggagaattgg gaccaatttg accctcagac agtaagaaaa   480

aaatgactta tattcttctg cagtaccgcc ctggccacga tatcctcttc aaggggagga   540

aacctggcct cctgagggaa gtataaatta taacaccatc ttacagctag acctgttttg   600

tagaaaagga ggcaaatgga gtgaagtgcc atatttacaa actttctttt cattaaaaga   660

caactcgcaa ttatgttaac agtgtgattt gtgttcctac acggaagccc tcagattcta   720

ctccccaccc ccggcatctc ccctgaatcc ctccccaact tatt   764

<210> 31

<211> 800

<212> DNA

<213> MSRV

<400> 31
tgtccgctgt gctcctgatc cagcacaggc gcccattgcc tctcccaatt gggctaaagg   60

22

```
cttgccattg ttcctgcaca gctaagtgcc tgggttcatc ctaatcgagc tgaacactag    120

tcactgggtt ccacggttct cttccatgac ccatggcttc taatagagct ataacactca    180

ctgcatggtc caagattcca ttccttggaa tccgtgagac caagaacccc aggtcagaga    240

acacaaggct tgccaccatg ttggaagcag cccaccacca ttttggaagc ggcccgccac    300

tatcttggga gctctgggag caaggacccc caggtaacaa tttggtgacc acgaagggac    360

ctgaatccgc aaccatgaag ggatctccaa agcaattgga aatgttcctc ccaaggcaaa    420

aatgccccta agatgtattc tggagaattg ggaccaatct gaccctcaga cagtaagaaa    480

aaaaatgact tatattcttc tgcagtaccg cctggccacg gatatcctct tcaaggggga    540

gaaacctggc ctcctgaggg aagtataaat tataacacca tcttacagct agacctgttt    600

tgtagaaaag gaggcaaatg gagtgaagtg ccatatttac aaactttctt ttcattaaaa    660

gacaactcgc aattatgtaa acagtgtgat ttgtgtccta caggaagccc tcagatctac    720

ctccctaccc cggcatctcc ctgactcctt ccccaactaa taaggaccca cttcagccca    780

aacagtccaa aaggacatag                                                800
```

<210> 32

<211> 65

<212> PRT

<213> MSRV

<400> 32

```
Pro Met Ala Ser Asn Arg Ala Ile Thr Leu Thr Ala Trp Ser Lys Ile
1               5                   10                  15


Pro Phe Leu Gly Ile Arg Glu Thr Lys Asn Pro Arg Ser Glu Asn Thr
            20                  25                  30


Arg Leu Ala Thr Met Leu Glu Ala Ala His His His Phe Gly Ser Ser
        35                  40                  45


Pro Pro Leu Ser Trp Glu Leu Trp Glu Gln Gly Pro Gln Val Thr Ile
    50                  55                  60


Trp
65
```

<210> 33

<211> 26

<212> DNA

<213> MSRV

<400> 33
tcatgcaact gcactcttct ggtccg   26

<210> 34

<211> 28

<212> DNA

<213> MSRV

<400> 34
tcttgcacta acctccactg tccgttgg   28

<210> 35

<211> 28

<212> DNA

<213> MSRV

<400> 35
atcccccagt aacaatttgg tgaccacg   28

<210> 36

<211> 31

<212> DNA

<213> MSRV

<400> 36
tcgggtctaa gagggtactt cctttggtag g   31

<210> 37

<211> 25

<212> DNA

<213> MSRV

<400> 37
ttacgcaggt ctcagggatg agctt   25

<210> 38

<211> 33

<212> DNA

<213> MSRV

<400> 38
cggcagtagc agtcttagta tctgaagcag tta   33

<210> 39

<211> 28

<212> DNA

<213> MSRV

<400> 39
ggtacggagg gtttcatgta gttttgag   28

<210> 40

<211> 1247

<212> DNA

<213> MSRV

<220>

<221> misc_feature

<222> (1240)..(1240)

<223> n = a, g, c or t/u

<220>

<221> misc_feature

<222> (1246)..(1246)

<223> n = a, g, c or t/u

<400> 40

```
atgggcagca gccatcatca tcatcatcac agcagcggcc tggtgccgcg cggcagccat       60
atggctagca tgactggtgg acagcaaatg ggtcggatcc tagaacgtat tctggagaat      120
tgggaccaat gtgacactca gacgctaaga aagaaacgat ttatattctt ctgcagtacc      180
gcctggccac aatatcctct tcaagggaga gaaacctggc ttcctgaggg aagtataaat      240
tataacatca tcttacagct agacctcttc tgtagaaagg agggcaaatg gagtgaagtg      300
ccatatgtgc aaactttctt ttcattaaga gacaactcac aattatgtaa aaagtgtggt      360
ttatgcccta caggaagccc tcagagtcca cctccctacc ccagcgtccc ctccccgact      420
ccttcctcaa ctaataagga ccccccttta acccaaacgg tccaaaagga gatagacaaa      480
ggggtaaaca atgaaccaaa gagtgccaat attccccgat tatgcccccct ccaagcagtg      540
agaggaggag aattcggccc agccagagtg cctgtacctt tttctctctc agacttaaag      600
caaattaaaa tagacctagg taaattctca gataaccctg acggctatat tgatgtttta      660
caagggttag gacaatcctt tgatctgaca tggagagata taatgttact actaaatcag      720
acactaaccc caaatgagag aagtgccgct gtaactgcag cccgagagtt tggcgatctt      780
tggtatctca gtcaggccaa aataggatg acaacagagg aaagaacaac tcccacaggc      840
cagcaggcag ttcccagtgt agaccctcat tgggacacag aatcagaaca tggagattgg      900
tgccacaaac atttgctaac ttgcgtgcta gaaggactga ggaaaactag gaagaagcct      960
atgaattact caatgatgtc cactataaca cagggaaagg aagaaaatct tactgctttt     1020
ctggacagac taagggaggc attgaggaag catacctccc tgtcacctga ctctattgaa     1080
ggccaactaa tcttaaagga taagtttatc actcagtcag ctgcagacat tagaaaaaac     1140
ttcaaaagtc tgcctaagct tgcggccgca ctcgagcacc accaccacca ccactgagat     1200
ccggctgcta acaaagcccg aaaggaagct gagttgggtn gtggcna                   1247
```

<210> 41

<211> 1186

<212> DNA

<213> MSRV

<400> 41

```
atggctagca tgactggtgg acagcaaatg ggtcggatcc tagaacgtat tctggagaat        60

tgggaccaat gtgacactca gacgctaaga aagaaacgat ttatattctt ctgcagtacc       120

gcctggccac aatatcctct tcaagggaga gaaacctggc ttcctgaggg aagtataaat       180

tataacatca tcttacagct agacctcttc tgtagaaagg agggcaaatg gagtgaagtg       240

ccatatgtgc aaactttctt ttcattaaga gacaactcac aattatgtaa aaagtgtggt       300

ttatgcccta caggaagccc tcagagtcca cctccctacc ccagcgtccc ctccccgact       360

ccttcctcaa ctaataagga cccccctta acccaaacgg tccaaaagga gatagacaaa       420

ggggtaaaca atgaaccaaa gagtgccaat attccccgat tatgccccct ccaagcagtg       480

agaggaggag aattcggccc agccagagtg cctgtacctt tttctctctc agacttaaag       540

caaattaaaa tagacctagg taaattctca gataaccctg acggctatat tgatgtttta       600

caagggttag acaatcctt tgatctgaca tggagagata taatgttact actaaatcag       660

acactaaccc caaatgagag aagtgccgct gtaactgcag cccgagagtt tggcgatctt       720

tggtatctca gtcaggccaa caataggatg acaacagagg aaagaacaac tcccacaggc       780

cagcaggcag ttcccagtgt agaccctcat tgggacacag aatcagaaca tggagattgg       840

tgccacaaac atttgctaac ttgcgtgcta gaaggactga ggaaaactag gaagaagcct       900

atgaattact caatgatgtc cactataaca cagggaaagg aagaaaatct tactgctttt       960

ctggacagac taagggaggc attgaggaag catacctccc tgtcacctga ctctattgaa      1020

ggccaactaa tcttaaagga taagtttatc actcagtcag ctgcagacat tagaaaaaac      1080

ttcaaaagtc tgcctaagct tgcggccgca ctcgagcacc accaccacca ccactgagat      1140

ccggctgcta acaaagcccg aaaggaagct gagttggctg gtggca                      1186
```


<210> 42

<211> 2030

<212> DNA
```

<213>    MSRV

<400>    42
atggccctcc cttatcatac ttttctcttt actgttctct tacccccttt cgctctcact        60

gcaccccctc catgctgctg tacaaccagt agctcccctt accaagagtt tctatgaaga       120

acgcggcttc ctggaaatat tgatgcccca tcatatagga gtttatctaa gggaaactcc       180

accttcactg cccacaccca tatgccccgc aactgctata actctgccac tctttgcatg       240

catgcaaata ctcattattg dacagggaaa atgattaatc ctagttgtcc tggaggactt       300

ggagccactg tctgttggac ttacttcacc cataccagta tgtctgatgg gggtggaatt       360

caaggtcagg caagagaaaa acaagtaaag gaagcaatct cccaactgac ccggggacat       420

agcacccctabcccctacaa aggactagtt ctctcaaaac tacatgaaac cctccgtacc       480

catactcgcc tggtgagcct atttaatacc accctcactc ggctccatga ggtctcagcc       540

caaaacccta ctaactgttg gatgtgcctc cccctgcact tcaggccata catttcaatc       600

cctgttcctg aacaatggaa caacttcagc acagaaataa acaccacttc cgttttagta       660

ggacctcttg tttccaatct ggaaataacc catacctcaa acctcacctg tgtaaaattt       720

agcaatacta tagacacaac cagctcccaa tgcatcaggt gggtaacacc tcccacacga       780

atagtctgcc taccctcagg aatattttt gtctgtggta cctcagccta tcattgtttg       840

aatggctctt cagaatctat gtgcttcctc tcattcttag tgcccctat gaccatctac        900

actgaacaag atttatacaa tcatgtcgta cctaagcccc acaacaaaag agtacccatt        960

cttccttttg ttatcagagc aggagtgcta ggcagactag gtactggcat tggcagtatc      1020

acaacctcta ctcagttcta ctacaaacta tctcaagaaa taaatggtga catggaacag      1080

gtcactgact ccctggtcac cttgcaagat caacttaact ccctagcagc agtagtcctt      1140

caaaatcgaa gagctttaga cttgctaacc gccaaagag ggggaacctg tttatttta       1200

ggagaagaac gctgttatta tgttaatcaa tccagaattg tcactgagaa agttaaagaa      1260

attcgagatc gaatacaatg tagagcagag gagcttcaaa acaccgaacg ctggggcctc      1320

ctcagccaat ggatgccctg ggttctcccc ttcttaggac ctctagcagc tctaatattg      1380

ttactcctct ttggaccctg tatctttaac ctccttgtta agtttgtctc ttccagaatt      1440

gaagctgtaa agctacagat ggtcttacaa atggaacccc agatggagtc catgactaag      1500

atccaccgtg gaccctgga ccggcctgct agcccatgct ccgatgttaa tgacattgaa       1560

ggcacccctc ccgaggaaat ctcaactgca caaccctac tatgccccaa ttcagcggga       1620

28

```
agcagttaga gcggtcatca gccaacctcc ccaacagcac ttgggttttc ctgttgagag      1680

ggggactga gagacaggac tagctggatt tcctaggcca acgaagaatc cctaagccta      1740

gctgggaagg tgactgcatc cacctctaaa catggggctt gcaacttagc tcacacccga      1800

ccaatcagag agctcactaa aatgctaatt aggcaaaaat aggaggtaaa gaaatagcca      1860

atcatctatt gcctgagagc acagcgggag ggacaaggat cgggatataa acccaggcat      1920

tcgagccggc aacggcaacc ccctttgggt cccctccctt tgtatgggcg ctctgttttc      1980

actctatttc actctattaa atcttgcaac tgaaaaaaaa aaaaaaaaa                  2030


<210>  43

<211>  2055

<212>  DNA

<213>  MSRV


<400>  43
cagcaacccc ctttgggtcc cctcccattg tatgggagct ctgttttcac tctatttcac       60

tctattaaat catgcaactg cactcttctg gtccgtgttt tttatggctc aagctgagct      120

tttgttcgcc atccaccact gctgtttgcc accgtcacag acccgctgct gacttccatc      180

cctttggatc cagcagagtg tccgctgtgc tcctgatcca gcacaggcgc ccattgcctc      240

tcccaattgg gctaaaggct tgccattgtt cctgcacagc taagtgcctg ggttcatcct      300

aatcgagctg aacactagtc actgggttcc acggttctct tccatgaccc atggcttcta      360

atagagctat aacactcact gcatggtcca agattccatt ccttggaatc cgtgagacca      420

agaaccccag gtcagagaac acaaggcttg ccaccatgtt ggaagcagcc caccaccatt      480

ttggaagcag cccgccacta tcttgggagc tctgggagca aggaccccag gtaacaattt      540

ggtgaccacg aagggacctg aatccgcaac catgaaggga tctccaaagc aatgggaaac      600

gttccccccg aggcaaaaat gccctagaa cgtattctgg agaattggga ccaatgtgac      660

actcagacgc taagaaagaa acgatttata ttcttctgca gtaccgcctg gccacaatat      720

cctcttcaag ggagagaaac ctggcttcct gagggaagta taaattataa catcatctta      780

cagctagacc tcttctgtag aaaggagggc aaatggagtg aagtgccata tgtgcaaact      840

ttctttttcat taagagacaa ctcacaatta tgtaaaaagt gtggtttatg ccctacagga      900

agccctcaga gtccacctcc ctaccccagc gtccctccc cgactccttc ctcaactaat      960
```

29

```
aaggacccccc ctttaaccca aacggtccaa aaggagatag acaaaggggt aaacaatgaa    1020

ccaaagagtg ccaatattcc ccgattatgc cccctccaag cagtgagagg aggagaattc    1080

ggcccagcca gagtgcctgt acctttttct ctctcagact taaagcaaat taaaatagac    1140

ctaggtaaat tctcagataa ccctgacggc tatattgatg ttttacaagg gttaggacaa    1200

tcctttgatc tgacatggag agatataatg ttactactaa atcagacact aaccccaaat    1260

gagagaagtg ccgctgtaac tgcagcccga gagtttggcg atctttggta tctcagtcag    1320

gccaacaata ggatgacaac agaggaaaga acaactccca caggccagca ggcagttccc    1380

agtgtagacc ctcattggga cacagaatca gaacatggag attggtgcca caaacatttg    1440

ctaacttgcg tgctagaagg actgaggaaa actaggaaga agcctatgaa ttactcaatg    1500

atgtccacta taacacaggg aaaggaagaa aatcttactg cttttctgga cagactaagg    1560

gaggcattga ggaagcatac ctccctgtca cctgactcta ttgaaggcca actaatctta    1620

aaggataagt ttatcactca gtcagctgca gacattagaa aaaaacttca aaagtccgtc    1680

ttaggctcgg aacaaaactt agaaaccccta ttgaacttgg caacctcggt tttttataat    1740

agagatcagg aggagcaggc agaatgggac aaatgggata aaaaaaaaag ggccaccgct    1800

ttagtcatgg ccctcaggca agcggacttt ggaggctctg gaaaagggaa aagctgggca    1860

aataggaagc ctaatagggc ttgcttccag tgcggtctac aaggacactt taaaaaagat    1920

tgtccaaata gaaataagcc gccccccttgt ccatgccccct tacgtcaagg gaatcactgg    1980

aaggcccact gccccagggg atcaagatac tctgagtcag aagccattaa ccagatgatc    2040

cagcagcagg actga                                                     2055


<210>   44

<211>   1197

<212>   DNA

<213>   MSRV


<400>   44
ggacccgtag tatggggtaa tccccctccgg gaaaccaagc cccagtactc agaagaagaa      60

atagaatggg gaacctcacg aggacatggt ttcctcccct caggatggct agccactgaa     120

gaaggaaaaa tacttttgct ggcagctaac caatggaaat tacttaaaac ccttcagcaa     180

accttccact taggcattga tagcacccat cagatagcca aatcattatt tactggacca     240
```

30

```
ggccttttca aaactatcaa gcagatagtc agggcctgtg aagtgtgcca aagaaataat      300

cccctgcctt atcgccaagc tccttcagga gaacaaagaa caggcaatta cccaagagaa      360

gactggcaac tagattttat ccacatgcca aaatcacagg gatttcagtg tctactagtc      420

tgggtagata ctttcactgg ttgggcagag gccttcccct gtaggacaga aaagttccaa      480

gaggtaataa aggcactagt tcatgaagta attcccagat tcggacttcc ctgaggctta      540

cagagtgaca atggtcctgc tttcaaggcc acagtaaccc agggagtatc ccaggcgtta      600

ggtatagaat atcacttaca ctgcacctag aggccacaat cctcagggaa ggttgagaaa      660

atgaaaacac tcaaacgaca tctaaacaag ctaacccagg aaacccacct cgcatggtct      720

gctctgttgt ctatagcctt actaagaatc caaaactctc cccaaaaggc aggacttagc      780

ccatacagaa tgctgtatgg acggtccttc ctaaccaatg accttctgct tgaccaagag      840

atggccaact tagttgcaga catcacctcc ttagccaaat atcaacaagt tcttaaaaca      900

ttacaaggag cctgtccccg agaggaggga aaagaaatat tccaccctgg tgtcatggta      960

ttagtcaagt cccttccctc taattcccca tccctagaca catcctgggg aggaccctac     1020

ccagtcattt tatctatccc aactgcggtt aaagtggctg gagtggagtc ttggatacat     1080

cacactcgaa tcaaaccctg gatactgccg aaggaacccg aaaatccagg ggacaacgct     1140

agctatttct ttgaacctct agaggatctg tgcctgctct tcaagcaaca accgtga        1197
```

<210> 45

<211> 1718

<212> DNA

<213> MSRV

<400> 45
```
gagaatagca gcataagttg gctggcagaa gtagggaaag acagcaagaa gtaaagaaaa       60

aaaggagaaa gtcagagaaa gaaaaaaaga gaggaagaaa caaagaagaa cttgaagaga      120

gaaagaagta gtaaagaaaa aacagtatac cctattcctt aaaagccag ggtaaatttc      180

tgtctaccta gccaaggcat attcttctta tgtggaacat caacctatat ctgcctcccc      240

actaactgga caggcaccag aaccttagtc tttctaagtc ccaacattaa cattgcccca      300

ggaaatcaga ccctattggt acctgtcaaa gctaaagtcc gtcagtgcag agccatacaa      360

ctaatatccc tatttatagg gttaggaatg gctactgcta caggaactgg aatagccggt      420
```

31

```
ttatctactt cattatccta ctaccataca ctctcaaaga atttctcaga cagtttgcaa      480

gaaataatga aatctattct tactttacaa tcccaattag actctttggc agcaatgact      540

ctccaaaacc gccgaggccc acacctcctc actgctgaga aaggaggact ctgcaccttc      600

ttaggggaag agtgttgttt ttacactaac cagtcaggga tagtacgaga tgccacctgg      660

catttacagg aaagggcttc tgatatcaga caatgccttt caaactctta taccaacctc      720

tggagttggg caacatggct tcttccattt ctaggtccca tggcagccat cttgctgtta      780

ctcacctttg ggccctgtat ttttaagctt cttgtcaaat ttgtttcctc taggatcgaa      840

gccatcaagc tacagatggt cttacaaatg gaaccccaaa tgagttcaac taacaacttc      900

taccaaggac ccctggaacg atccactggc acttccacta gcctagagat tcccctctgg      960

aagacactac aactgcaggg cccccttcttt gcccctatcc agcaggaagt agctagagcg     1020

gtcatcggcc aaattcccaa cagcagttgg ggtgtcctgt ttagagggg gattgaagag       1080

tgacagcctg ctggcagcct cacagccctc gttggatctc agtgcctcct cagccttggt     1140

gcccactctg gccgtgcttg aggagccctt cagcctgcca ctgcactgtg ggagcctctt     1200

tctgggctgg acaaggccgg agccagctcc ctcagcttgc agggaggtat ggagggagag     1260

atgcaggcgg gaaccaggc tgcgcatggc gcttgcgggc cagcatgagt tccaggtggg       1320

cgtgggctcg gcgggcccca cactcgggca gtgaggggct tagcacctgg gccagacaga     1380

tgctgtgctc aacttcttcg ctgggcctta gctgccttcc ccgtggggca gggctacggg     1440

aacatgcagc ctgcccatgc ttgagccccc caccccgccg tgggttcytg cacagcccaa     1500

gcttcccgga caagcaccac cccttatcca cggtgcccag tcccatcaac cacccaaggg     1560

ttgaggagtg cgggcacaca gcgcgggatt ggcaggcagt tccacttgcg gccttggtgc     1620

gggatccact gcgtgaagcc agctgggctc ctgagtctgg tggggacttg gagaatcttt     1680

atgtctagct aagggattgt aaatacacca atcagcac                             1718
```